

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 02:18:14 ; Search time 67.56 Seconds

(without alignments)
512.021 Million cell updates/sec

Title: US-09-719-748-2

Perfect score: 1846

Sequence: 1 MEPEKQKVEDFDIGELG.....TEEDIARRKALHPRRSSTS 360

Scoring table:

BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_71:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1248	67.6	1423	1 I37275	death-associated p
2	787	42.6	1435	2 T32930	hypothetical prote
3	703.5	38.1	1176	2 JN0583	myosin-light-chain
4	694	37.6	1147	2 A59307	myosin-light-chain
5	685.5	37.1	1906	1 S68235	myosin-light-chain
6	665.5	36.1	2783	2 T34416	hypothetical prote
7	651.5	35.3	371	2 UC7733	death-associated p
8	650	35.2	6658	2 T13931	prolectin - fruit
9	621.5	33.7	451	2 A49128	twichin-like prot
10	605	32.8	608	2 A35021	myosin-light-chain
11	604	32.7	610	2 A28798	myosin-light-chain
12	589	31.9	1211	2 T27522	hypothetical prote
13	584.5	31.7	6831	2 A88852	proctein unc-22 (lm
14	584.5	31.7	6839	2 S57242	twichin (similar
15	584.5	31.7	7160	2 T27935	hypothetical prote
16	547	29.6	301	1 A40811	myosin-light-chain
17	541	29.3	26926	1 T38344	titin, cardiac mus
18	536	29.0	516	1 J00270	Ca2+/calmodulin-de
19	535	29.0	509	2 B44412	calmodulin-depende
20	534	28.9	530	2 D44412	Ca2+/calmodulin-de
21	532	28.8	474	2 TVRTCA	Ca2+/calmodulin-de
22	532	28.8	502	2 T52637	Ca2+/calmodulin-de
23	530.5	28.7	370	1 S57347	Ca2+/calmodulin-de
24	530.5	28.7	374	1 S50193	Ca2+/calmodulin-de
25	530	28.7	473	1 A53036	Ca2+/calmodulin-de
26	527.5	28.6	469	1 S17656	Ca2+/calmodulin-de
27	526.5	28.5	533	1 A34366	Ca2+/calmodulin-de
28	510.5	27.7	348	2 T37321	Ca2+/calmodulin-de
29	510	27.6	538	2 T08874	calcium-dependent

30	507.5	27.5	518	1 B46619	Ca2+/calmodulin-de
31	507.5	27.5	556	2 JC5636	Ca2+/calmodulin-de
32	506	27.4	520	2 C84774	probable calcium-d
33	503	27.2	540	1 T01989	calcium-dependent
34	502.5	27.2	484	2 T05650	calcium-dependent
35	502	27.2	527	1 A31908	Ca2+/calmodulin-de
36	500.5	27.1	518	1 S43845	Ca2+/calmodulin-de
37	500.5	27.1	544	2 D84550	probable calmodul
38	496.5	26.9	573	2 T09940	calcium-dependent
39	493.5	26.7	708	2 T23616	hypothetical prote
40	492.5	26.7	560	2 T46189	calcium-dependent
41	490.5	26.6	533	1 S56652	calcium-dependent
42	489.5	26.5	487	1 S71770	calcium-dependent
43	489.5	26.5	610	1 A49082	calcium-dependent
44	489	26.5	531	2 D85059	probable calcium d
45	488	26.4	520	2 F85059	probable calcium d

ALIGNMENTS

RESULT	1	
I37275	death-associated protein kinase (EC 2.7.1.-) - human	
N:Alternate names: calmodulin-dependent protein kinase homology; DAP kinase		
C:Species: Homo sapiens (man)		
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 10-Jul-1998		
C:Accession: I37275; S39269		
R:Deiss, L.P.; Feinstein, E.; Berissi, H.; Cohen, O.; Kimchi, A.		
G:Genes Dev. 9, 15-30, 1995		
A:Title: Identification of a novel serine/threonine kinase and a novel 15-kD protein		
A:Reference number: A55614; MUID:95129831		
A:Accession: I37275		
A:Molecule type: mRNA		
A:Residues: 1-1423 <RES>		
A:Cross-references: EMBL:X76104; NID:9434846; PID:9434847		
C:Genetics:		
A:Gene: GDB:DAPK1; DAPK		
A:Cross-references: GDB:555932; OMIM:600831		
A:Map position: 9q34.1-9q34.1		
C:Function:		
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-thre		
A:Pathway: apoptosis		
A>Note: activity is calmodulin dependent		
C:Superfamily: death-associated protein kinase; ankyrin repeat homology; protein kin		
C:Keywords: apoptosis; ATP; calmodulin binding; phosphotransferase; serine/threonine		
F:11-267/Domain: protein kinase homology <KIN>		
F:19-27/Region: protein kinase Arp-binding motif		
F:285-308/Region: calmodulin binding #status predicted		
F:370-402/Domain: ankyrin repeat homology <AN1>		
F:403-435/Domain: ankyrin repeat homology <AN2>		
F:436-468/Domain: ankyrin repeat homology <AN3>		
F:470-502/Domain: ankyrin repeat homology <AN4>		
F:503-535/Domain: ankyrin repeat homology <AN5>		
F:536-568/Domain: ankyrin repeat homology <AN6>		
F:569-601/Domain: ankyrin repeat homology <AN7>		
F:602-634/Domain: ankyrin repeat homology <AN8>		
F:42,64,139,141/Active site: Lys, Glu, Asp, Lys #status predicted		
Query Match	67.6%	Score 1248; DB 1; Length 1423;
Best Local Similarity	66.5%	Pred. No. 1.1e-44;
Matches 236; Conservative	60;	Mismatches 43; Indels 16; Gaps 3;
OY	1	MEPEKQKVEDFDIGELSGGFAIVKCRKSTGLEAYAKFKRQSRASRGVSRRE 60
DB	1	MTYFROENVDDYDTGSELSSGGFAVYKCRKSTGLGYAKFKRRTSSRGVSRRED 60
OY	61	IEREVSLRQVLLHNNVTTLHDVYENRTDVVHILEVSGGLFDFLACKESLSEEARSTFT 120
DB	61	IEREVSLRQVLLHNNVTTLHDVYENRTDVVHILEVSGGLFDFLACKESLSEEARSTFT 120
OY	121	KQLLDGVNVTYHTTKKIAHFDLKPENIMLDKNIPRPHIKLDFGLAHIEGVEKKNIFGT 160

C:Accession: JN0583; P:JN0490
R:Kobayashi, H.; Inoue, A.; Mikawa, T.; Kuwayama, H.; Hotta, Y.; Masaki, T.; Ebashi, T. Biochem. 112, 786-791, 1992
A:Title: Isolation of cDNA for bovine stomach 15kDa protein exhibiting myosin light
A:Reference number: JN0583; MUID:93203148
A:Accession: JN0581
A:Molecule type: mRNA
A:Residues: 1-1176 <C03>
A:Cross-references: GB:557131; NID:g298638; PIDN:AAB25794.1; PID:g298639
A:Experimental source: stomach
A:Accession: FND0490
A:Molecule type: protein
A:Residues: 44-55;721-728;828-851;1002-1019 <K02>
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; fibronectin type I
C:Keywords: ARP; calmodulin binding; phosphotransferase
E:3370-430/Domain: immunoglobulin homology <IMM1>
F:723-980/Domain: protein kinase homology <KIN>
F:731-739/Region: protein kinase ARP-binding motif
F:1083-1144/Domain: immunoglobulin homology <IMM2>

Query Match	38.1%;	Score 703.5;	DB 2;	Length 1176;
Best Local Similarity	42.5%;	Pred. NO. 2.6e-22;		
Matches 149;	Conservative 62;	Mismatches 117;	Indels 23;	Gaps 7.

Qy	6	QOKHEFVYDIBGELSGOGFATYKCKREKSTGLEIYAKFKIKKQJASRKRGSRELEEV	63
Dp	718	EOKVSDPYDIEERLGSCKFQOYRVEKTEKGTGIMAGFEKFRASAK-----EKENIROEI	771
Qy	66	SILRQVLAHHVILTHDOYENRDUVILITELSGGELFDFLAQE--SLSESEATSTIKOIL	124
Dp	772	SIMCLTHPLVOCVDHFEERKANTIVLWELTSGGELFEYIIDEDELHREBCKIKMKRIS	831
Qy	125	DGVNVLHTFKRIARFDLKPENIMILDKNIDIPHIKLIDFGLAHEIDGYEKNIFCTPEFV	184
Dp	832	EGVEYIKHOGIVHDLDKPENIMCVNKT--GTRIKLIDFGLARLBNAGSLKLEFCTPEFV	889
Qy	185	APELVANEPIGLLEADMKSTGVITYILLSSAPSLQGTKEPLANTSVSYDDEDEFESHT	244
Dp	890	APELVANEPIGVAETDMKSTICVICYILLVSGISLSPMGNDNETLANTVATSKATWDDDAFDEI	949
Qy	245	SELKADETIRKLILVKEETKRKLITOEALRHPI--TPVNDQOAMVRRSVNLENFRKQYVR	303
Dp	950	SDDAKDEISNLKKDKMKRNLCTOGLHPMLMDTKNMEA-----KLSKDMKKRYKARR	1004
Qy	304	RWKLSSEFVSLCNHILRSLM-----KYNHLRDEDDLANCESDPEEIOIAR	347
Dp	1005	KMOCTGAANVAIRGLRSLMAAISGLSGRKSSTGSPISPL--NAEKLSBEDVSO	1054

RESULT 4
A59307
myosin-light-chain kinase (EC 2.7.1.117), smooth muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
A:Accession: A59307; A1674; B1674; A40210
R:Gallagher, P.J.; Herring, B.P.; Griffin, S.A.; Stull, J.T.
J. Biol. Chem. 266, 23936-23944, 1991
A:Title: Molecular characterization of a mammalian smooth muscle myosin light chain
A:Reference number: A1674; MUID:92084694
A:Accession: A59307
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1147 <GB>
A:Cross-references: GB:M6233; NID:q165703; PIDN:AA73093.1; PID:q165704
A:Experimental source: dev stage Adult; sex Female; tissue type smooth muscle

A: Molecule type: mRNA
A: Residues: 1-738, 'RC', 741-1147 <GA4>
A: Cross-references: GB: M76233
A: Note: the sequence is revised in GenBank entry RABSMMLCKR, release 115, (PIDN: AAA7)
A: Accession: BA1674

Query Match	37.68;	Score 694;	DB 2;	Length 1147;
Best Local Similarity	41.68;	Pred. NO. 6.2e-22;		
Matches 146;	Conservative 63;	Mismatches 120;	Indels 22;	Gaps 6

```
7          304 RAKLSISIVSLCNHLTRSL-----KKVHLPDEDLRNCESDTEEDIAR   347
           ::::| |::|| |||:::
976 KMQGTNAVRATIGRLSSMAMISGLSGRKSTGSPITLAETLEEDYSQ    1026
```

Reference number: A37099; MUID:90361738
Accession: A37099
Molecule type: mRNA

F:1459-1467/Region: protein kinase ATP-binding motif
E:1750-1966/Product: telokin (kinase-related protein KRP) (from 2.7 kb transcript) #
#:1808-1869/Domain: Immunoglobulin homology <IM3>

```

Oy 125 DGAVNLHTKKAAHFDLKPENIMLBDKNIPRIPIKLIDGLAHEIDEDGVEFFNIFGTPEFV 184
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 1560 EGVEIHKQGIYHLDLKPENIMCVAKT--GTSIKLIDGLARRLSESAGSLVLFGTPEFV 1617

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A:Residues: 1-371 <MAT>
A:Accession: PC7178
A:Molecule type: protein
A:Residues: 227-371 <MA2>
C:Comment: This kinase, a novel calcineurin homologous protein (CHP) binding protein involved in the transfer of Na+/H+ exchanger 1 process and in some apoptotic events.
C:Genetics:
A:Gene: drak2
C:Keywords: apoptosis

Query Match          35.3%; Score 651.5; DB 2; Length 371;
Best Local Similarity 46.8%; Pred. No. 1.3e-20;
Matches 133; Conservative 52; Mismatches 84; Indels 15; Gaps 7;

QY 3 PRKQKVEDEPYD-GEELSGGQFAIVKCKREKSTGSLYAKFIKKROSRRSGVS-REE 60
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 22 PMKTEFNPNNEITTPRELGRGKFAAVRQCLSKSTGGEYAKFKLKKR----RGDQCRAE 76
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 IEREVSIL--ROYLHNVTITLDVYENKRDVYHIELVSGGELEDFELAAK--ESLSEE 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 ILHEIIVLEIARSCPH--VINLHEVYETAETIIVLYAAGGELFNCLDELMEMVSEND 134
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 ATSGFIQIILDGVNVLHTKTAHFDLKDPENTIMLDKNIPRIKILIDGLAHEIDSGVEK 175
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 VIKRIKQILEGVNHLHQNNTIVHLDLKPQNI-LTSSIVPLDDIKIVDQSMKIKGNASELR 193
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 176 NIGCTPEFVAPETVNYNEPFLGELDMWSIGVITYILLGASPELGDQETKLTANTISVSVD 235
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 194 EIMGTPEYLAPELILNYDPIITATDMNIGIAYMLLHTSPFGEEDNQETYLINISQVNV 253
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 FDEEFESHTELANDKFTIKLLVKETRRKLTIQEALRHFWITPPVD 279
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 254 YSEMFSSVQLANDFIQSLLVKNPKRPRTESSCLSHWLOOMD 297

```

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RESULT      8
T13931
projectin - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13931
R:Daley, J.: Southgate, R.; Ayme-Southgate, A.
J. Mol. Biol. 279, 201-210, 1998
A>Title: Structure of the Drosophila projectin protein: Isoforms and implication for
A:Reference number: 217815; MUID:98300339
A:Accession: T13931
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6658 <DAL>
A:Cross-References: EMBL:AF047475; NID:g3337430; PID:g3337431; PIDN:AAC27550.1
C:Genetics:
A:Gene: projectin
A:Cross-References: FlyBase:FBgn005666
A:Map position: 4
A:Note: Intron positions not resolved (Incomplete sequence)
C:Keywords: muscle

```

```

Matches 197:   Conserved: 27
QY      6 QOKVEFDYDIGEELGSGOFAIVKKCKREKSTGLEVAAMFIKKROSRASRGVSREIEREV    65
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     5707 QOSVTDYDKDLELDELGTAGFVGVRHCRBSRNGINIAAFIPVSHS-----VEKDITREI    5760

QY      66 SIHQVLHNVTILHDVENRTDVVHLIELVSGEELD-FLAOKESLSSEETATSEIKOL    124
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     5761 DIMQLNHHOKILINDHAFFEDDEDMILLIEPFGSELGERITAEGVMTAEVIYNMRDIC    5820

QY      125 DGVNVLTHTKTAAHDLKPENIMLDKNPIRIPIKILIDGLAHNEIDEGVFKNIGCTPEFV    184
          ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Db 5821 EGRHMEQNIILHLDIKPENIMQOTRS--STNVKLIIDFGIATRLDNPENVKITTTGAERG 5878
Oy 185 ABEIYNVEPLGLEADPMMSIGVITYILLSCASPLFGTKQETANTITSVYDDEEFFSHT 244
Db 5879 ABEIYNREPVGTYTDMAMGAVLYLVLSGLSPAGNDQOTLKNVACWDFLESFKYI 5938
Oy 245 SELAKDFIKLLVETKRTKLTIOEALRHPWIPVDN--QOAMVRRSVNLNFRQOYR 302
Db 5939 SEEAADFIRKLVLNKKEMKTAHECLLHPWLGDHSAMKOEINRDRYLAVREKLKRYED 5998
Oy 303 -RRWKLFSIVSLCNHLTRSLMK 325
Db 5999 FERFLPIGRLSVSLRKLMEK 6022

RESULT 9
twitclhn-like protein - California sea hare (fragment)
C:Species: Aplysia californica (California sea hare)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 17-Nov-2000
C:Accession: S49128; A53923
R:Heierhorst, J.; Probst, W.C.; Vilim, F.S.; Buku, A.; Weiss, K.R.
submitted to the EMBL Data Library, February 1994
A:Description: Autophosphorylation of molluscan twitclhn and interaction of its kinase
A:Reference number: S49128
A:Accession: S49128
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-451 <HER>
A:Cross-references: EMBL:Z30161; NID:9509412; PIDN:CA82911.1; PID:9509413
R:Heierhorst, J.; Probst, W.C.; Vilim, F.S.; Buku, A.; Weiss, K.R.
J. Biol. Chem. 269, 21086-21093, 1994
A:Title: Autophosphorylation of molluscan twitclhn and interaction of its kinase domain
A:Reference number: A53923; MUID:94342273
A:Accession: A53923
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 5-372 <HE2>
A:Cross-references: GB:Z20161
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP
F:45-302/Domain: protein kinase ATP-binding motif
F:53-61/Region: protein kinase ATP-binding motif

Query Match 33.7%; Score 621.5; DB 2; Length 451;
Best Local Similarity 46.0%; Pred. No. 2.6e-19;
Matches 125; Conservative 50; Mismatches 88; Indels 9; Gaps 3;

Oy 5 KQOKVEDPDIQBELSGQFAIVKCKREKSTGLEVAAPFKRKQSRASRGVREIEERE 64
Db 39 KQSGCDYIDILEELSGAFGVVHRCVKAATGVEFAKFIN-----TPYPLDKYVKN 92
Oy 65 VSILROVLNHNVTLLADVENRTDVVHILELVSGELFDFLAQKE-SLSEEAATSFIKOT 123
Db 93 ISIMQNLNHPKILNLDAREKDYDVLLELPSGLGELFDRIAAEDYKMSAEVATINMRQA 152
Oy 124 LQGVNLTHTKTAHPRLKAEINMLDKNIPRIKILIDGLAHEIDGVEFKKIFSTPER 183
Db 153 CEGKLMHMEHSIVHLDIKPENIMCETKK--ASSVKIIDFGIATRLKLPDELIVKTTATAER 210
Oy 184 VAPETYNVPEPLGLEADPMMSIGVITYILLSCASPLFGTKQETANTITSVYDDEEFFSH 243
Db 211 APEIYDRPVGFTYDMMAGVLYLVLSGLSPFAGEDDLETQNVKRCMDWEDDAFSS 270
Oy 244 TSELAKDFIKLLVETKRTKLTIOEALRHPWI 275
Db 271 VSPKADFIRKLVLNKKEMKTAHECLLHPWLGDHSAMKOEINRDRYLAVREKLKRYED 302

RESULT 10
A55021
myosin-light-chain kinase (EC 2.7.1.117), skeletal muscle - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 24-Sep-1999
C:Accession: A35021; A05120; A25830
R:Herring, B.P.; Stull, J.T.; Gallagher, P.J.
J. Biol. Chem. 265, 1724-1730, 1990
A:Title: Domain characterization of rabbit skeletal muscle myosin light chain kinase.
A:Reference number: A35021; MUID:90110242
A:Accession: A35021
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-608 <HER>
A:Cross-references: GB:J05194; NID:9165505; PIDN:AAA31400.1; PID:9165506
R:Takio, K.; Blumenthal, D.K.; Fellman, A.M.; Walsh, K.A.; Krebs, E.G.; Titani, K.
Biochemistry 24, 6028-6037, 1985
A:Title: Amino acid sequence of an active fragment of rabbit skeletal muscle myosin
A:Reference number: A05120; MUID:86104095
A:Accession: A05120
A:Molecule type: protein
A:Residues: 237-604 <TA2>
R:Takio, K.; Blumenthal, D.K.; Walsh, K.A.; Titani, K.; Krebs, E.G.
Biochemistry 25, 8049-8057, 1986
A:Title: Amino acid sequence of rabbit skeletal muscle myosin light chain kinase.
A:Reference number: A25830; MUID:87101105
A:Accession: A25830
A:Molecule type: protein
A:Residues: 2-336, 'K', 337-604 <TA2>
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; muscle; phosphotransferase; serine/threonine-specific protein kinase
F:595-552/Domain: protein kinase homology <KIN>
F:303-311/Region: protein kinase ATP-binding motif

Query Match 32.8%; Score 605; DB 2; Length 608;
Best Local Similarity 40.4%; Pred. No. 1.6e-18;
Matches 124; Conservative 63; Mismatches 106; Indels 14; Gaps 5;

Oy 17 EELSGQFAIVKCKREKSTGLEVAAPFKRKQSRASRGVREIEEREVSILROVLNHN 76
Db 301 EALGGKFGAVCTCTEKSTGLKLAAYIKKOTK-----DKEMYLEIVMQLNHRNL 354
Oy 77 ITLHDVYENFTDVVHILELVSGELFDFLAQKE-SLSEEAATSFIKOILDGVNLTAKTI 135
Db 355 IQLYAAIETPHEIIVLEFVEYEGGELFERIVDEDVHILEVTQVNFVROICDIGILFMHMRV 414
Oy 136 AHFDIKPENIMLDKNIPRIKILIDGLAHEIDGVEFNITGTPEFVAPETYNPEPLG 195
Db 415 LHLIDKPEINILCVNTGHL--VKIIDGLARRYNPMKILKVNCTGPEFLSPEVAVNDQIS 472
Oy 196 LEADPMMSIGVITYILLSCASPLFGDTQKQETANTITSVYDDEEFFSHTSELAKDFIRKL 255
Db 473 DKTDMSLGVITYTLLSGLSPLFGDDDTETLNNVLSGNMVFDEETPEAVSDEAKDFVSNL 532
Oy 256 LVKTRKRLTIOEALRHPWITPVNDQAMVR--ESVYNLENFRKOYVRRMKLSFSIVS 313
Db 533 IVKEGARMSAQAOLAPWLNILAEKAKRCNRLKQISL---KKYLMKRRMKKNFIAYS 589
Oy 314 LCNHLTR 320
Db 590 AANRFKK 596

RESULT 11
A28798
myosin-light-chain kinase (EC 2.7.1.117), skeletal muscle - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jan-1989 #sequence_revision 12-Jan-1989 #text_change 19-Dec-1997
C:Accession: A28798; A60441
R:Roush, C.L.; Kennelly, P.J.; Giaccum, M.B.; Helman, D.M.; Scott, J.D.; Krebs, E.G.
J. Biol. Chem. 263, 10510-10516, 1988
A:Title: Isolation of the cDNA encoding rat skeletal muscle myosin light chain kinase
A:Reference number: A28798; MUID:88273159
A:Accession: A28798
A:Molecule type: mRNA

Query Match	31.2%	Score 589;	DB 2;	Length 1211;
Best Local Similarity	41.2%	Pred. No. 1.4e-17;		
Matches 140;	Conservative 48;	Mismatches 112;	Indels 40;	Gaps 8;
QY	8	KVEDFDIGCELTGSCFALVKKCRKREKSGTLEAAAFITTKRQSRASRGVSGSEETIERVSI	67	
b	40	KPFLTVQVKKLLDGGFFGKYCVITIEEKGKFAAFIK-----IKKEDRAAEVEREVSII	93	

Query Match	31.7%	Score 584.5	DB 2	Length 6831
Best Local Similarity	42.0%	Pred No. 1e-16	Mismatches 98	Indels 9
Matches 115	Conservative	52		Gaps 3
OY	5	KOOKVEDFDIGEBELSSGGFAIVKCKREKSTGTEIAKTKRKQSAKRGVSREREIE	64	
Db	5926	KHHVLDHNDHIDHEELTSGFAGVVRHTRATGNNFAKFLVMPRHES-----DKETVKE	5979	
OY	65	VSTLRQVLHNHTLTLDVYENFRDVNHLIELVSGGELFDPLAQKES-LSEEAFTSFKOI	123	
Db	5980	IQMSVLRHPTLVNLDALFDQDNEVMYIEFMSGGELFEKVAEDHNKMSDEAVELMYROY	6039	
OY	124	LDCVNLHTTKKIAHFEDLKPRNIMLKDKNPIRIPIKILDGLANIEDEGVKIFGPRP	183	
Db	6040	CKELICHNHNYYVLDLKRPENIMFTKR--SNEKILDFCSLTJLHDPKQSVKTTGTAEF	6097	
OY	184	VAREIYVVEEDIGLEADMMISGIVTYTLLISGASPFADTQKOTLANITSVYDDEEFFSH	243	
Db	6098	AAEVAEAGKRVGYTUDMWSGVLSYLLISGSPFGGENDETLRNVKSCDMNDDSAFSG	6157	
OY	244	TSELADFTIKRLVYKTRKRLTQDALRHHMIP	277	
Db	6158	ISEDGKDFIKRLLDADENTKTHIQALEHMLTP	6191	

RESULT 14
S57242
twitchin [similarity] - *Caenorhabditis elegans*

N:Alternate names: myosin-regulating protein
N:Contains: protein kinase (EC 2.7.1.-)
C:Species: Caenorhabditis elegans
C:Date: 28-Oct-1995 #sequence, revision 24-Oct-1997 #text, change 20-Jun-2000
A:Accession: S57242; S07571, S06797; S57218; T27934; T28030
R:Benian, G.M.; I'Hernault, S.W.; Morris, M.E.
A:Description: Additional sequence complexity within twitching of *Caenorhabditis elegans*
A:Submitted to the EMBL Data Library, February 1993
A:Reference number: S57242
A:Accession: S57242
A:Molecule type: DNA
A:Residues: 1-6839 <BEN1>
A:Cross-references: EMBL:L10351
A:Experimental source: var. Bristol
R:Benian, G.
A:Submitted to the EMBL Data Library, November 1989
A:Reference number: S07571
A:Accession: S07571
A:Molecule type: DNA
A:Residues: 752-6839 <BEN2>
A:Cross-references: EMBL:X15423; NID:96897; PIDN:CAA3463.1; PID:96898
A:Experimental source: var. Bristol
R:Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
A:Title: Sequence of an unusually large protein implicated in regulation of myosin activity
A:Reference number: S06797; MUID:90044042
A:Accession: S06797
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 806-1175,1178-1998, 'Y', 2000-3040, 'I', 3042-3335, 'I', 3337-5693; 5696-6359, 'I', 6360-6361
A:Cross-references: EMBL:X15423
A:Experimental source: var. Bristol
R:Benian, G.M.; I'Hernault, S.W.; Morris, M.E.
A:Title: Additional sequence complexity in the muscle gene, unc-22, and its encoded protein
A:Reference number: S57218; MUID:93387664
A:Accession: S57218
A:Molecule type: DNA
A:Residues: 2-99,108-194, 'Q', 196-206; 374-468; 658-753 <BEN4>
A:Experimental source: var. Bristol
R:White, S.
A:Submitted to the EMBL Data Library, May 1996
A:Reference number: Z20442
A:Accession: Z27934
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'MGIPGKCKQ', 19-6839 <WIL>
A:Cross-references: EMBL:Z73897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a
A:Experimental source: clone ZK617
R:Harris, B.
A:Submitted to the EMBL Data Library, May 1996
A:Reference number: Z20458
A:Accession: T28030
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'MGIPGKCKQ', 19-6839 <WIL2>
A:Cross-references: EMBL:Z73899; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a
A:Experimental source: clone ZK829
C:Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
C:Genetics:
A:Gene: unc-22; CESP:ZK617.1a
A:Map position: 4
A:Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 600/3
152/3; 6691/3; 6776/1; 6808/3
C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; serine/threonine kinase
R:806-898, 899-990, 991-1083, 1084-1175, 1178-1273, 1474-1567, 1770-1864, 2066-2158, 2358-2450, 2451-2549, 2550-2648, 2649-2742, 2743-2838, 2839-2931, 2932-3026, 3027-3121, 3122-3216, 3217-3311, 3312-3406, 3407-3501, 3502-3596, 3597-3691, 3692-3786, 3787-3881, 3882-3976, 3977-4071, 4072-4166, 4167-4261, 4262-4356, 4357-4451, 4452-4546, 4547-4641, 4642-4736, 4737-4831, 4832-4926, 4927-5021, 5022-5116, 5117-5211, 5212-5306, 5307-5401, 5402-5496, 5497-5591, 5592-5686, 5687-5781, 5782-5876, 5877-5971, 5972-6066, 6067-6161, 6162-6256, 6257-6351, 6352-6446, 6447-6541, 6542-6636, 6637-6731, 6732-6826, 6827-6921, 6922-7016, 7017-7111, 7112-7206, 7207-7301, 7302-7396, 7397-7491, 7492-7586, 7587-7681, 7682-7776, 7777-7871, 7872-7966, 7967-8061, 8062-8156, 8157-8251, 8252-8346, 8347-8441, 8442-8536, 8537-8631, 8632-8726, 8727-8821, 8822-8916, 8917-9011, 9012-9106, 9107-9201, 9202-9296, 9297-9391, 9392-9486, 9487-9581, 9582-9676, 9677-9771, 9772-9866, 9867-9961, 9962-10000
F:1274-1372, 1373-1473, 1474-1574, 1575-1675, 1676-1776, 1777-1877, 1878-1978, 1979-2079, 2080-2180, 2181-2281, 2282-2382, 2383-2483, 2484-2584, 2585-2685, 2686-2786, 2787-2887, 2888-2988, 2989-3089, 3090-3190, 3191-3291, 3292-3392, 3393-3493, 3494-3594, 3595-3695, 3696-3796, 3797-3897, 3898-3998, 3999-4099, 4100-4200, 4201-4301, 4302-4402, 4403-4503, 4504-4604, 4605-4705, 4706-4806, 4807-4907, 4908-5008, 5009-5109, 5110-5210, 5211-5311, 5312-5412, 5413-5513, 5514-5614, 5615-5715, 5716-5816, 5817-5917, 5918-6018, 6019-6119, 6120-6220, 6221-6321, 6322-6422, 6423-6523, 6524-6624, 6625-6725, 6726-6826, 6827-6927, 6928-7028, 7029-7129, 7130-7230, 7231-7331, 7332-7432, 7433-7533, 7534-7634, 7635-7735, 7736-7836, 7837-7937, 7938-8038, 8039-8139, 8140-8240, 8241-8341, 8342-8442, 8443-8543, 8544-8644, 8645-8745, 8746-8846, 8847-8947, 8948-9048, 9049-9149, 9150-9250, 9251-9351, 9352-9452, 9453-9553, 9554-9654, 9655-9755, 9756-9856, 9857-9957, 9958-10000
E:5940-6197/Domain: protein kinase homology <KIN>
E:5948-5956/Region: protein kinase ATP-binding motif
E:5971/Active site: Lys #status predicted

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Query Match          31.7%; Score 584.5; DB 2; Length 6639;
Best Local Similarity 42.0%; Pred. No. 1e-16;
Matches 115; Conservative 52; Mismatches 98; Indels 9; Gaps 3;

OY      5 KQAKVEDPYDGEELGSGSOFALVKKCKREKSTGLEVAFAFKKRQSRASRGVSREIERE 64
        | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |
Db       5934 KHDHVLHDHYDIHEELGTAFGVHVHTERATGNNAAFVMTPRHS-----DKETVAKE 5987
        | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |

OY      65 VSILROVLHHNVITLADYVENRTDVNHLLELVSGGELFDPLAQOKES-LSEEBATSFIKOI 123
        : : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Cj:Cross-references: EMBL:Z73897; PIDs:CAA98065.1; GSPDB:GNU00022; CESP:ZK617.lb
OY      5988 IQTMSVLAHRPTLVNLHDAFEDDENEMWITYEFMSGEGELEKKADEHNKMSDEEAVEYMROY 6047
        : : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
OY      124 LDGVNYLTHTTKRIAHDLAPENIMLLDKNIPIPHIKLIDFGLAHLEDGVERKNIFGPREF 183
        : : : : : | | | | | | | | | | : | : | : | : | : | : | : |
Db       6048 CKGLCHMHENNTVHLDLPENIMFTTKR--SNELKLIDFGTLAHLDPKQSKVYTGTAEF 6105
        : : : : : | | | | | | | | | | : | : | : | : | : | : | : |

OY      184 VAPENVTEPRLGLEADMMSIGVTIYLISGASPFLGDTKOETLANITSVSYDFDEEFESH 243
        ||| : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       6106 AAPEVAEEKPGVGXYTADMSVGYLSYILLSGPSFGENDDELRVNKSCDMNMDSARSG 6165
        ||| : : | : | : | : | : | : | : | : | : | : | : | : | : |

OY      244 TSELAKDFIRKLIVKETRKRLTIQDALNRPTTP 277
        || | | | | | | | : | : | : | : | : | : | : | : | : |
Db       6166 ISEGDGDFIRKLLADPNTRMTHQALETWPWLP 6199
        || | | | | | | | : | : | : | : | : | : | : | : | : |

RESULT 15
T27935
hypothetical protein ZK617.lb - Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
CjAccession: T27935; T28031
RjWhite, S.
Submitted to the EMBL Data Library, May 1996
A:Reference number: Z20442
A:Accession: T27935
A>Status: preliminary; translated from GR/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-7160 <WLL>
A:Cross-references: EMBL:Z73897; PIDs:CAA98065.1; GSPDB:GNU00022; CESP:ZK617.lb
A:Experimental source: clone ZK617
RjHarris, B.
Submitted to the EMBL Data Library, May 1996
A:Reference number: Z20458
A:Accession: T28031
A>Status: preliminary; translated from GR/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-7160 <WTZ>
A:Cross-references: EMBL:Z73899; PIDs:CA98082.1; GSPDB:GNU00022; CESP:ZK617.lb
A:Experimental source: clone ZK629
CjGenetics:
A:Gene: CESP:ZK617.lb
A:Map position: 4
A:Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3,
1067/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097/1; 7129/3
CjSuperfamily: twitchin, fibronectin type III repeat homology, immunoglobulin homology

Query Match          31.7%; Score 584.5; DB 2; Length 7160;
Best Local Similarity 42.0%; Pred. No. 1.e-16;
Matches 115; Conservative 52; Mismatches 98; Indels 9; Gaps 3;

OY      5 KQAKVEDPYDGEELGSGSOFALVKKCKREKSTGLEVAFAFKKRQSRASRGVSREIERE 64
        | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |
Db       6255 KHDHVLHDHYDIHEELGTAFGVHVHTERATGNNAAFVMTPRHS-----DKETVAKE 6308
        | | | | | | | | | | : | : | : | : | : | : | : | : | : | : |

OY      65 VSILROVLHHNVITLADYVENRTDVNHLLELVSGGELFDPLAQOKES-LSEEBATSFIKOI 123
        : : : : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       6309 IQTMSVLAHRPTLVNLHDAFEDDENEMWITYEFMSGEGELEKKADEHNKMSDEEAVEYMROY 6368
        : : : : : | : | : | : | : | : | : | : | : | : | : | : | : |

OY      124 LDGVNYLTHTTKRIAHDLAPENIMLLDKNIPIPHIKLIDFGLAHLEDGVERKNIFGPREF 183
        : : : : : | | | | | | | | | | : | : | : | : | : | : | : |

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Db 6369 CKGCGHMHENNNYVHLDLKPENIMEFTKK--SNEKLIDEGFLAHLDKPDQSKQVTTGTAEF 6426

QY 184 VAPETVNEPGLGEADPMWSGVTYITLLTSGAPFGDTPQOEFLAITSVSDPDEEFSH 243

Db 6427 AAFPEAECKFPFGYITDMWSGVSLTLLSGLSFGSGENDEFLRVKSCDMMDSAEFG 6486

QY 244 TSELAKDFIRKLKLVKTRKTRITQELARHPWTP 277

Db 6487 TSDGKDFIRKLKLLADNPNTMTIHQALEHFWLP 6520

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